

Figure 1A

1 CAAGCACTGTGCTAAAGTGTTTTTCATATGTCATGAAAGTTGTGCCAGAAAATTATGGT 60
 61 TTGAACATGGGCAGTTTTCTCCTACCGTCAGCTATATCCAAGCATCACATGAAGTGGGA 120
 121 GATCTGGCAGCTCTGTGTATTTTCAGTCAAGTTCCACAATGAAACCTGACAATAATGGTAA 180
 181 AAACCAATACGGACATCTGAGTAACTGGGGAATTGGCCTGCCTTGCACTGTAGCTTGATG 240
 241 GAAGATTGGATATAGACGAGTTGATTATATTTTATGAAGTAGCAGCTCACTACCATCCAC 300
 301 CATCCAGGGTTTAAACTACTTTTTCAGCATCACTTCACCTGTGGACTCTTATACATTTTG 360
 361 ATTTCTTGGGGGAAAAATACTGGGATAAGAGGAGGTCATTTTTAAAGTTAGCATCCT 420
 421 TTTCCCTTTCTTACAAGTTGATCCAAAGGATAAGGCTGTGACTCCATTGGATTGCACCTT 480
 481 TAAATCAAAATAGCAGCAGCAGAAGAAAGGACAATGGCTCTGAGTGGAACTGTAGTCG 540
 1 M A L S G N C S R 9
 541 TTATTATCCTCGAGAACAAGGTCGCGCAGTTCCCAACTCTCTCCCTGAGTGTGATAGAGCT 600
 10 Y Y P R E Q G S A V P N S F P E V V E L 29
 601 GAATGTCGGGGGTCAAGTTATTTTACTCGCCATTCCACATTGATAAGCATCCCTCATTC 660
 30 N V G G Q V Y F T R H S T L I S I P H S 49
 661 CCTCCTGTGAAAAATGTTTCCCCCAAGAGAGACACGGCTAATGATCTAGCCAAGGACTC 720
 50 L L W K M F S P K R D T A N D L A K D S 69
 721 CAAGGGAAGGTTTTCATTGACAGAGATGGATTCTTGTTCGGTTATATCTGGACTATCT 780
 70 K G R F F I D R D G F L F R Y I L D V L 89
 781 CAGGGACAGCAGGTGGTCTGCTGATCACTTTCCAGAAAAAGGAAGACTGAAAAGGGA 840
 90 R D R Q V V L P D H F P E K G R L K R E 109
 841 AGCTGAATACTTCCAGCTCCAGACTTGGTCAAACCTCCTGACCCCGGATGAAATCAAGCA 900
 110 A E Y F Q L P D L V K L L T P D E I K Q 129
 901 AAGCCAGATGAATTCTGCCACAGTGACTTTGAAGATGCCTCCAAGGAAGCGACACAAG 960
 130 S P D E F C H S D F E D A S Q G S D T R 149
 961 AATCTGCCCCCTTCTCCCTGCTCCCTGCCGACCGCAAGTGGGGTTTCATTACTGTGGG 1020
 150 I C P P S S L L P A D R K W G F I T V G 169

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Figure 1B

| | | |
|------|--|------|
| 1021 | TTACAGAGGATCTCGACCTTGGGCAGAGAGGGACAGGCAGATGCCAAGTTTCGGAGAGT | 1080 |
| 170 | Y R G S C T L G R E G Q A D A K F R R V | 189 |
| 1081 | TCCCCGAGTTTGTGTTTGTGGAAGGATTTCTTGGCAAAAGAAGTCTTGGAGAAACTTT | 1140 |
| 190 | P R I L V C G R I S L A K E V F G E T L | 209 |
| 1141 | GAATGAAAGCAGAGACCCCTGATCGAGCCCCAGAAAGATACACCTCCAGATTTTATCTCAA | 1200 |
| 210 | N E S R D P D R A P E R Y T S R F Y L K | 229 |
| 1201 | ATTCAAGCACCTGGAAAGGGCTTTTGATATGTTGTCTCAGAGTGTGGATTCCACATGGTGGC | 1260 |
| 230 | F K H L E R A F D M L S E C G F H M V A | 249 |
| 1261 | CTGTAACCTCCTGGTGACAGCATCTTTTCATCAACCAATATACAGATGACAAGATCTGGTC | 1320 |
| 250 | C N S S V T A S F I N Q Y T D D K I W S | 269 |
| 1321 | AAGCTACACTGAATATGTCTTCTACCGTGAGCCTTCCAGATGGTCAACCTCACACTGCGA | 1380 |
| 270 | S Y T E Y V F Y R E P S R W S P S H C D | 289 |
| 1381 | TTGCTGCTGCAAGAATGGCAAAGGTGACAAAGAAGGGGAGAGCGGCACGCTTTCGAATGA | 1440 |
| 290 | C C C K N G K G D K E G E S G T S C N D | 309 |
| 1441 | CCTCTCCACATCTAGCTGCGACAGCCAGTCTGAGGCCAGCTCTCCCCAGGAGACGGTCAT | 1500 |
| 310 | L S T S S C D S Q S E A S S P Q E T V I | 329 |
| 1501 | CTGTGGTCCCCTGACACGCCAGACCAACATCCAGACTCTGGACCGTCCCATCAAGAAGGG | 1560 |
| 330 | C G P V T R Q T N I Q T L D R P I K K G | 349 |
| 1561 | CCCTGTCCAGCTGATCCAACAGTCAGAGATGCGGCGGAAAAGCGACTTACTCCGGATTCT | 1620 |
| 350 | P V Q L I Q Q S E M R R K S D L L R I L | 369 |
| 1621 | GACTTCAGGCTCCAGGGAATCGAACATGAGCAGCAAAAAAAAAAGCTGTAAAGAAAAGCT | 1680 |
| 370 | T S G S R E S N M S S K K K A V K E K L | 389 |
| 1681 | CTCAATTGAGGAGGAGCTGGAGAAATGTATCCAGGATTTCTTAAAAAAAATTCAGAA | 1740 |
| 390 | S I E E E L E K C I Q D F L K K K I P D | 409 |
| 1741 | TCGGTTTCTTGAGAGAAAAACATCTTGGCAATCTGAACTTTAAAGGAAGTATCATCTATA | 1800 |
| 410 | R F P E R K H P W Q S E L L R K Y H L | 428 |
| 1801 | AGGGAGGGCTGGGGGCGGGGAAAAAAGAGTCAATTTGAAATTAACTCATAA | 1860 |
| 1861 | AAGGAATTCATATTTTAAAGGAAAAAATACAATAATGATGCACATTTCTTAGAACACA | 1920 |
| 1921 | ATAGTCCATTGATATACTACTGCTACTTTACCTAGTTCACCTTAACATGTAAATCCACA | 1980 |

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Figure 1C

1981 GGGTAGATTTCTTCTTAGATGTGGAAGTACAAGAAAATCTTTTCTAGTTATTTGTTTGTT 2040
 2041 TACTTCGTCCCATGTGCTAACTATCTTATATATAATGAGAGCCAGCTACGTAAAAAGTAGC 2100
 2101 TGAGAGGCCTTGGGAGTCATTTATCCCAAACCTGGGTTTTTCTCTCATCCTTCTACCTCC 2160
 2161 CTCTTTTGAATGAGGGTATGGTAGAAAAAGATCTGGCCCAATGGCATAAGTTTGAATTT 2220
 2221 TTAATTTTGGTTTTTCTTTTGTTTATGGGGTTGGGGGAATGGCAGATTATATGACTT 2280
 2281 TTCACTCAAATCTATATGTGCCAGTTTATATTGACTCCGTATGCATGAGTATTTGTGCAA 2340
 2341 CACAAGCACAACCTAAGTATGTATATACACATGACGCACACGATGCCAGGCCTAGACCTC 2400
 2401 CCAAGGGCTGTGCTCCTGCTCCAGCAGCCCTCTCTTAGAATATTTAGATGGATGAGCT 2460
 2461 TCTGACTCTTTCTTAAAAATCTTTTGGGAAGATTCCAGCCCTTCTTCAACAACACTTTC 2520
 2521 TAACATCAAATGACTCTCATCATCAACAAATTGATTCCTTATTGTGAAATTAATACCTT 2580
 2581 CAGGCTCCATTTTACTGCTTTGCTCTTTGTCTGCATTAAGAGAGGATGAGGAGAGCTGGT 2640
 2641 CAAACATTCCCTTGTTTAAAAAATCAAACATTATATCCACAAAATTTTCTGCTAAATG 2700
 2701 ACTCCCACTCAGCCTTCTCTACCCCTGAATGAATTATCACCCCTTTTCTCCATGTTTCA 2760
 2761 GAGTTCTTACTGCCACAGTTTAATGGTGTGGCCTTTCCACATAATCCACATTAAAGTTCT 2820
 2821 GTGTTCTGTGTTGTGTGGAACCTAAGGACAACACACAGTACTTGAATAAGGGTCCGGCC 2880
 2881 TTTTGTGTTGTTTAGAGAAAGTTGTATTCCACACACAACCTAATAATTTCTTATAAAAAAT 2940
 2941 TTTAAACTACAAGCTACATTTTACTTGCTTGTAGCCGTTTTTGTGTCCTTTGGGATT 3000
 3001 CGGGCTTTGGCTGTGCCATGCTAGGATTAGCTGTGCTATTTTATGATGTCTGTAAACA 3060
 3061 ACCCAACAAGGTAACTGAAGCTCCAGAGTTAAGGTTTCAGATTCTTAAATGAACTATCT 3120
 3121 TTTTCAATTACATCTTGACTTGTATAGACACAGCCAAAAAGAACTGTTAATAGCCATCC 3180

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[illegible]

Figure 2A

| | | | |
|------------|-------|-----------------------------------|--------------------------|
| 1 | | | 50 |
| K+betaM2 | (1) | -----MALSGNCSRYYPREGSAVPNS | PEPVVELNVGGGVYFTRHSTLIS |
| AAP558201 | (1) | ----- | MPETTELNVGGVYPTTLATLQ |
| CAA20329.1 | (1) | -----MTSVEDVITLNVGGVYPTTLATLQ | |
| Y34129 | (1) | -----MDNGDWGYMTD | PVTLNVGCHLITTSLSLTTR |
| Y34125 | (1) | MSRPLITRSPASPLXNQGIPTPAQLTKSNAPVH | LVGGHMTSSLSLTTR |
| | | 51 | 100 |
| K+betaM2 | (46) | IPHSLLWKMFPSP--KRDTANDLAKDSKGRFF | HRDCEFLRRVILDYDRDRQ |
| AAP558201 | (24) | DKSTLLAEFFG----EGRDSLAKDSKGRFF | HRDGVLRVILDFLRDKA |
| CAA20329.1 | (27) | ETDTLLANIASGSLSEDEQANVILP | PGTLFVDRDGLPAZVILHFLRTDK |
| Y34129 | (33) | YPPDSMLGAMFGG---D--FPDARDPPGNYE | HRDCEPLRRVILNLFRTSE |
| Y34125 | (51) | YPPSRIGNIPDG---T-EPIVLDLSLKQHYE | HRDCEQMRVILNLFRTSK |
| | | 101 | 150 |
| K+betaM2 | (94) | UVLPDHCPEKGRDKREAEYFQLPDIVKLLTPDE | IKQSPDEFCHSDPFEDAS |
| AAP558201 | (69) | LHLDEGCEPQRQLRENEHFKLTANPCERSE | DAR----- |
| CAA20329.1 | (77) | LSLEEGCEAEVARKDENDFYHLERESTLLSN | ASIS-PRPR----- |
| Y34129 | (77) | LTLELDEKEFDLIRKEADFYDEPLTQCLNDP | KPLY----- |
| Y34125 | (96) | LLLEPDRKDYTLDEEAKYFQLQPMLEMERW | KQDR----- |
| | | 151 | 200 |
| K+betaM2 | (144) | QGSDFRICPPSSLLPDRKWGFITVGYRGSCTLR | EGQADAKFRVPRIL |
| AAP558201 | (105) | -----PP-----GCITVGYRGS | PQFGGLADVKFRKILRIL |
| CAA20329.1 | (117) | -----TANGYNTITSGAETGGYITLGYRGT | FAFGREGQADVKFRKILRIL |
| Y34129 | (113) | -----PMDTFEEVVELSSTRKLSKYSNP | VAVITITQLITTK |
| Y34125 | (132) | -----ETGRFSRPECCLVVRVNPDLGERIT | LSGDKSLDEEVE |
| | | 201 | 250 |
| K+betaM2 | (194) | VCGRVTSLEAEVFCETLNESRDPDR-APERY | TSRFYLKFKHLERAPMLSE |
| AAP558201 | (137) | VCGRVTAQCEVFQDTLNESRDPDHGGIDRY | TSRFLLKHCMLQAPFNLHD |
| CAA20329.1 | (162) | VCGRVTLCEVFADTLNESRDPGG--PDGCE | |
| Y34129 | (149) | VHSLDEGISNYFITKWNKHMMDIRD | --CQVSFTPGCDYHQEVSLEVHLM |
| Y34125 | (169) | PEIGDVHNCNSVNAGWNHDSHIVIR---- | FPLNGYCHLNSVQMLERLQQ |
| | | 251 | 300 |
| K+betaM2 | (243) | CGEHMVAENSSVTASFIN-----QYTD | DKIWSSYTEYFYREPSRWSPSH |
| AAP558201 | (187) | HGRFMAAGSCGSGTAGSAAEPKPGVDTE | ENRNHNHYNEFVPIRD |
| CAA20329.1 | (191) | ----- | ----- |
| Y34129 | (196) | EYITKQGFTTIRNTRVHHMSERANENTV | HNHWTCRLARKTDD |
| Y34125 | (213) | RGEEIVGSCGGGVDSQSFSEYVLRREL | RTPRVPSVIRIKQDEPL |
| | | 301 | 350 |
| K+betaM2 | (288) | CDCCCKNGKGDKEGESGTSCNDLSTSSCD | SQSEASSPQETVICGPVTRQT |
| AAP558201 | (229) | ----- | ----- |
| CAA20329.1 | (191) | ----- | ----- |
| Y34129 | (238) | ----- | ----- |
| Y34125 | (257) | ----- | ----- |
| | | 351 | 400 |
| K+betaM2 | (338) | NIQTLDRLPIKKGVPVLIQQSEMRRKSD | LLRLITSGSRESNMSSKKKAVKE |
| AAP558201 | (229) | ----- | ----- |
| CAA20329.1 | (191) | ----- | ----- |
| Y34129 | (238) | ----- | ----- |
| Y34125 | (257) | ----- | ----- |

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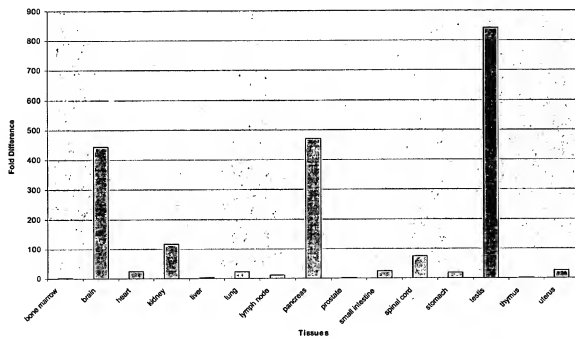
D0076 NP

Figure 2B

| | 401 | 441 |
|------------------|---|-------|
| K+betaM2 (388) | KLSIEEELEKCIQDFLKKKIPDRFPERKHPWQSELLRKYHL | |
| AAP558201 (229) | ----- | ----- |
| CAA20329.1 (191) | ----- | ----- |
| Y34129 (238) | ----- | ----- |
| Y34125 (257) | ----- | ----- |
| Consensus (401) | | |

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Figure 3



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Figure 4.

| Protein | Genbank ID | Identities | Similarities |
|--|---------------|------------|--------------|
| Human potassium channel K+Hnov28 | gi Y34129 | 31% | 41% |
| Drosophila CG10830 protein | gi AAF55820.1 | 52% | 66% |
| Caenorhabditis K+ channel tetramerisation domain | gi CAA20329.1 | 42% | 51% |
| Human potassium channel K+Hnov27 | gi Y34125 | 32% | 41% |

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